

Replacement Sheet

Gene III leader sequence in KO7 helper phage

SEQ ID NO. 1	GTG AAA AAA TTA TTA TTC GCA ATT CCT TTA GTT GTT CCT TTC TAT TCT CAC TCC GCT
SEQ ID NO. 2	V K K L L L F A I P L V V P F Y S H S A

Gene III leader sequence in KO7kpn helper phage

SEQ ID. NO. 3	GTG AAA AAA TTA TTA TTC GCA ATT CCT TTA GTG <u>GTA CCT</u> TTC TAT TCT CAC TCC GCT
SEQ ID. NO. 2	V K K L L L F A I P L V V P F Y S H S A

KpnI



Fig. 3B



Replacement Sheet

GR2-Myc domain coding sequence in GM-UltraHelper phage genome

SEQ ID. NO. 4
KpnI Gene III leader GR2
---TTAGTGGTACCTTTCTATTCTCACTCCGCT ACATCCCGCCTGGAGGGCCTACAGTCAGAAAAACCATCGCCTGCCGA

SEQ ID. NO. 5
- L V V P F Y S H S A T S R L E G L Q S E N H R L R
NotI

ATGAAGATCACAGAGCTGGATAAAGACTTGAAGAGGTCAACCATGCAGCTGCAGGACGTCGGAGGTTGC GCGGCCGCA
M K I T E L D K D L E E V T M Q L Q D V G G C A A A

Myc-tag BglII Gene III
GAACAAAACTCATCTCAGAAGAGGATCTG AGATCTGGAGGCGGT ACTGTTGAAAAGTTGTTTAGCAAAA---
E Q K L I S E E D L R S G G G T V E S C L A K -

Fig. 5B



Replacement Sheet

Trypsin cleavage sites at GR2-Myc domain on GM-UltraHelper phage

SEQ ID NO. 6

GR2 domain

T S R L E G L Q S E N H R L R M K I T E L D K D L E E V

Myc-tag

T M Q L Q D V G G C A A A E Q K L I S E E D L R S G G G

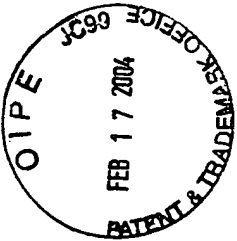
Fig. 5C



SEQ ID NO. 7

GGGGCGCAACGCAATTAATGTGAGTTAGTCTACTCATTAGCCACCCAGGCTTTACACTTTATGCTTCGGGCTCGTATGTGTGGAATTGTGAGCGGATACAATTTACCGGTTCTTTTAAGGAGGA
 ATTTAAAAATGAATACCTATTGCTACGGGAGCCGTGGATTGTTATTACTCGCGGCCACGCGCCATGCGGCCCTCTAGAGCGCCGCTGGAGGTGAGGAGAAGTCCCGGCTG
 TTTTGGAGGAGGAAACCGTGAATCGGAAAGAGGAGCGGTGTCCTGAACATCGGCATCAACTCCACTCTGTAGGAGTTGTAGACTTTATCCATACGACATACGACAGCTA
 CCGGACGAGGTCATCACCATCATCACTAATATGATCGACCTCGCCAAATATGCCCCATAGTAGCTGATTAACACTCTGCGCTCGTTTTACAACTGCTGCTGCTGGAAACACCTCCGCGCTA
 ACCCAACTTAATGCGCTTCGACGACATCCCCCTTTGCGCAGCTGGCCTAATAGCGAAGAGCGCCGACCGATCGCCTTCCCAACAGTTCGCGACCTGAATGCGGAATGGGACGCGCTGTAG
 CCGCGCGCATTAAGCGCGCGGGTGTGTGTGTAGCGGACGCTGACCTACATTCGCGCGCCCTTAGCGCCGCTTCTTCCTTCCTTCGCGCACGTTTCGCGGGCTTTCCCC
 GTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTAGTGCTTTAGGCGACCTCGACCCCAAATAACTGATTAGGGTGATGTTACGTAAGTGGGCCATCGCCCTGATAGACGGTTTCTT
 CGCGCCTTTGACGTTGGAGTCCAGCTCTTTAATAGTGAGCTCTGTTTCCAAATGGAACACACATCAACCCATCTCTCGTCTATTCTTTTGATTATATAGAGGATTTTGGCGATTTCGGCCTATTG
 GTTAAAAAATGAGTGTATTAACAAAAATTAACCGCAATTTAAACCAATATTAAGCTTTACAAATTTAGTGGGCACTTTTCGGGAAATTTGCGGGAACCCCTATTGTTTATTATTTCTAAAT
 GACTTCAAATATGATATCGCTCATAGACAAATAGACGAAACGCTGGTGAAGTAAAGATGCTGAAGATCAGTTGGTGCACGAGTGGGTTACATCGAACTGGAATCTCAACACGGGTGAAGTCTTGAGAGTTTTCG
 CGCGAAGAACGTTTCCNATGATGAGCACTTTTAAAGTTCTGCTATCTGGCCGGTATTATCCCGTATTGACCGCGGCAAGAGCAACTCGCTCGCCGATACACTTCTGTACACAGATCGAGGAC
 TTGAGTACTCACCACTACAGAAAGCATCTTAGCGATGGCATGACACTAAGAGAAATATGCACTGCTGCCATTAACCATAGTATGATCACTCGCTCGCCGATACACTTCTGTACACAGATCGAGGAC
 CGAAGGACATACCGCTTTTTCGCAACAACTAGGGGATCATGATACGCTCTGTTGGGAAACGGAGCTGAATGAGCCATACAAACGACGAGCTTACCTACGACATGCTTGACCAATG
 CGCAACGCTTGCGCAAACTTTAACTGGCGAACTACTTACTCTAGCTTCGCGGCAAAATTAATAGACTGGATGAGGGGATAAAGTGAAGCCCTCCGCTATCTACAGACGGGGAGTCAGGCAACTA
 CTGGTTTANTGTGTAAATCTGGAGCGGTGACGTGGGCTCTCGCGGTATCATTCGACACTGGGGCCAGATGGTAAGCCCTCCGCTATCTGAGTATCTACAGACGGGGAGTCAGGCAACTA
 TGGNTGAACGAATAGACAGATCGCTGAGTAGGTGCTCATGATTAAAGCATTTGTAAGCATTTGTAAGTAACTCTACAGACCAAGTTTACTCATATATATTTAGATTGATTAAAACTTCATTTTAAATTTAAAAAG
 ATCTAGTGTGAAGATCTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGGCTCAGCCGCTAGAAAGATCAAAAGGATCTTCCTTTGAGATCTCTTTTTCGCTGGC
 CGTAAATCTGCTTGCAACAAAAAACCCGTACCAAGCTGGGTGGTTTGTGTCCGGATCAAGAGCTACCACTCTTTTCCGAAAGTAACTGSCCTTCAGCAGCGGATACCAAAATCTG
 TCTCTCTAGTGTAGCGGTAGTTAGGCCACACTTCAAGAACTGTGACACCGCTCATACTCTGCTCTGCTAACTCTGTATACAGTGGCTGCTGCCAGTGGCAGTAAGTCTGCTCTTACCGGG
 TTGGACTCAAGACGATAGTTACCGGNTAAGCGCGAGCGGTGGGGCTGAAACGGGGGGTTTGTCGACACAGCCCGACGTTGGAGCGAACCACTACACCGAACTGAGTACCTACAGCGGTGAGCTATG
 AGAAAGCCCAACGCTCCGGAAGGGAGAAAGCGGACAGGATACCGGTAAAGCGGCGGTCGGAACAGGAGACGCGACGAGGAGCTTCAGGGGGGAAACCGCTCTGATCTTTATAGTCTCTGTCTG
 ATTTTGCCACCTCTGACTTAGGCTCGATTTTGTGATGCTGTACGGGGGCGGAGCCCTATGAAAAACGCCAGAACCGGCCCTTTACGGTTCCTGGCCCTTTTGTCTGGCCTTTTGTCTGCTAC
 ATGTTCTTCTCGGTTATCCCTGATTCTGTGGATACCGTATTATCCGCTTTTGTAGTGATGATACCTCGCTCAGCAACCGCCGACGCGGATCGTGAAGCGGACGCGGAGGAAAGCGGACG
 CGCGCCCAATACGCAAAACCGCTCTCCCGCGGCTTGGCCGATTCATTAATGAGCTGGCACAGCACTTCCCGACTGGAAAGCGGGCAGTGA

Fig. 9B



Replacement Sheet

Engineered gene III sequence in CM phage -- Nucleotide Sequence: SEQ ID. NO. 8;
Amino Acid Sequence: SEQ ID. NOS. 9 and 25

SEQ ID. NO. 8

KpnI Gene III leader Amber stop NotI Myc-tag BglII
---TTAGTGGTACCTTTCTATTCTCACTCCGCT TAGGCTTGCGGTGGTGGCGCCGACAGAACAAAACTCATCTCAGAAGAGGATCTGAGATCT AGATCTGGA

SEQ ID. NO. 9

- L V V P F Y S H S A * A C G G A A A E Q K L I S E E D L R S R S G

Gene III

GGCGGT ACTGTTGAAAGTTGTTTAGCAAAACCTCATACAGAAAATTCATTACTAAGTCTGGAAAGACGACAAAACTTTAGATCGTTACGCT-----
G G T V E S C L A K P H T E N S F T N V W K D D K T L D R Y A - -

Fig. 13B



SEQ ID NO. 10

[illegible]

Fig. 15B



Replacement Sheet

Engineered gene III Sequence in GMCT phage genome

SEQ ID. NO. 11

KpnI Gene III Leader

GR2 domain

--TTAGTGGTACCTTCTATCTCACTCCGCT ACATCCCGCTGGAGGGCCTACAGTCAGAAAACCATCGCCTGCGAATGAAGATCACAGAGCTGGATAAA

SEQ ID. NO. 12

-L V V P F Y S H S A T S R L E G L Q S E N H R L R M K I T E L D K
NotI Myc-tag

GACTTGAAGAGGTCACCATGCAGCTGCAGGACGTCGGAGGTGC GCGGCCGAGAACAAAACTGATCTCAGAAGAGGATCTGACGCGTGCT GGCGGC
D L E E V T M Q L Q D V G G C A A E Q K L I S E E D L T R A G G

CT domain of Gene III

GGCTCTGGTGGTCTGGTGGCGCTCTGAGGGTGGCGGCTCTGAGGGTGGCGGCTCTGAGGGTGGCGGTTCCGGTGGCGGCTCC
G S G G S G G S E G G S E G G S E G G S E G G S E G G S E G G S
GGTCCGGTGATTTGATGAAAAAATGGCAACGCTAATAAGGGGCTATGACCGAAATGCCGATGAAAACGCGCTACAGCTGACGCTAAAGGCAAA
G S G D F D Y E K M A N A N K G A M T E N A D E N A L Q S D A K G K
CTTGATTCTGCGCTACTGATTACGGTGTGCTATCGATGGTTTCATTTGGTACGTTTCCGGCCTTGCTAATGGTAATGGTGTACTGGTGATTTGCTGGC
L D S V A T D Y G A A I D G F I G D V S G L A N G N G A T G D F A G
TCTAATCCCCAATGGCTCAAGTCGGTGACGGTGATAATTCACCTTTAATGAATAATTCGGTCAATATTACCTTCCCTCAATCGGTTGAATGTCGC
S N S Q M A Q V G D G D N S P L M N N F R Q Y L P S L P Q S V E C R
CCTTTTGTCTTTGGCGCTGGTAAACCATATGAATTTCTATTGATTGTGACAAAATAAACTTATCCGTTGGTGCTTTTGGCTTTCTTTATATGTTGCCACC
P F V F G A G K P Y E F S I D C D K I N L F R G V F A F L L Y V A T

Ascl S/D

TTTATGTATGATTTTCTACGTTTGCTAACATACTGCGTAATAAGGAGTCTTAATAA GCGCGCCCAACAATTCACAGTAAGGAGGTTTAATAA ATGAAA
F M Y V F S T F A N I L R N K E S * M K

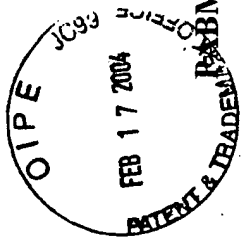
OmpA leader

BglII

Gene III

AAGACAGCTATTGGGATTGCAGTGGCACTGGCTGGTTTCGCTACCGTAGCGCAGGCT AGATCTGGAGGCGGT ACTGTTGAAAAGTTGTTTAGCAAAA---
K T A I A I A V A L A G F A T V A Q A R S G G G T V E S C L A K -

Fig. 19B



Replacement Sheet

PABMD1 vector: sequence from AgeI to Sall - Nucleotide Sequence: SEQ ID. NO. 13
Amino Acid Sequence: SEQ ID. NOS. 14 and 26

SEQ ID. NO. 13

lac promoter/lac O1 AgeI EP S/D
AATTGTGACGGGATAACAATTT ACCGGT TCTT TTAACCTTAG TAAGGAGG AATTAAAAA
P8 Leader HindIII XbaI
ATGAAAAAGTCTTTAGTCCTCAAGCCTCCGTAGCCGTGCTACCCCTCGTCCGATGCTAAGCTTCGCT TCTAGA

SEQ ID. NO. 14

M K K S L V L K A S V A V A T L V P M L S F A S R
SEQ ID. NO. 26

NotI	HA-tag	His-tag	Amber stop	BglII
CGGGCCCGCT	TATCCATACGACGTACCGACTACGCA	GGAGGT CATCACCATCATCACCAT	TAG	AGATCT
A A A	Y P Y D V P D Y A G G H H H H	*		R S
Gene 3				
GGAGGCGGT	ACTGTTGAAAGTTGTTTAGCAAAA	----- GCTAACATACTGCGTAATAAGGAGTCTTAA		GTCGAC
G G G	T V E S C L A K	----- A N I L R N K E S	*	
Sall				

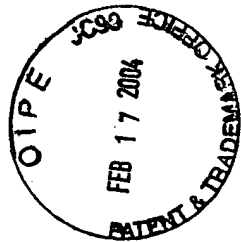
PABMD2 vector: sequence from AgeI to Sall

lac promoter/lac O1 AgeI EP S/D
AATTGTGACGGGATAACAATTT ACCGGT TCTT TTAACCTTAG TAAGGAGG AATTAAAAA
pelB Leader Nco I PstI XbaI
ATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGGGCCAGCCGCCCATGGCGCCCTGCAGGCCTCTAGA
M K Y L L P T A A A G L L L L A A Q P A M A A L Q A S R

SEQ ID. NO. 26

NotI	HA-tag	His-tag	Amber stop	BglII
CGGGCCCGCT	TATCCATACGACGTACCGACTACGCA	GGAGGT CATCACCATCATCACCAT	TAG	AGATCT
A A A	Y P Y D V P D Y A G G H H H H	*		R S
Gene 3				
GGAGGCGGT	ACTGTTGAAAGTTGTTTAGCAAAA	----- GCTAACATACTGCGTAATAAGGAGTCTTAA		GTCGAC
G G G	T V E S C L A K	----- A N I L R N K E S	*	
Sall				

Fig. 22B



Replacement Sheet

GR1 Sequence Range: 1 to 146

XbaI 10 20 30 40 50
SEQ ID. NO. 15
TCTAGAGGTGGAGGAGGTGAGGAGAAAGTCCCGGCTGTTGGAGAAGGAGAA
SEQ ID. NO. 16
S R G G G G E E K S R L L E K E N
60 70 80 90 100
CCGTGAAC TGGAAAAGATCATTTGCTGAGAAAGAGGAGCGGTGCTCTGAAC
R E L E K I I A E K E R V S E
110 120 130 140 AscI
TGCGCCATCAACTCCAGTCTGTAGGAGGTTGTTAATAGGCGCGGCC
L R H Q L Q S V G G C * *

GR2 Sequence Range: 1 to 140

XhoI 10 20 30 40 50
SEQ ID. NO. 17
TCTCGAGGAGGTGGTGGAAACATCCCGCCTGGAGGGCCTACAGTCAGAAAA
SEQ ID. NO. 18
S R G G G G T S R L E G L Q S E N
60 70 80 90 100
CCATCGCCTGCGAATGAAGATCACAGAGCTGGATAAAGACTTGAAGAGG
H R L R M K I T E L D K D L E E
110 120 130 NotI 140
TCACCATGCAGCTGCAGGACGTCGGAGGTTGCGCGGCCGC
V T M Q L Q D V G G C A A

Fig. 23



SEQ ID NO. 23

[illegible]

Fig. 25B

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SEQ ID NO. 24

Fig. 26B